

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 21:07:08 ; Search time 26 Seconds  
(without alignments)  
86.143 Million cell updates/sec

Title: US-09-659-737A-2

Perfect score: 293  
Sequence: 1 HRDIKAGNILLIKETIHDDI.....EMHRTTKMSTAGTYAMNAP 54

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	81.6	394	1	M3K9_HUMAN
2	216	73.7	954	1	M3K9_HUMAN
3	124.5	42.5	859	1	M3K9_HUMAN
4	124.5	42.5	888	1	M3K9_MOUSE
5	124.5	42.5	888	1	M3K9_MOUSE
6	108.5	37.0	1478	1	BCK1_YEAST
7	101	34.5	589	1	SHK2_SCHPO
8	100	34.1	328	1	KRA6_MOUSE
9	100	34.1	367	1	RML_AVT11
10	100	34.1	450	1	RML_AVEVR
11	100	34.1	765	1	KRA6_HUMAN
12	100	34.1	806	1	RML_CHICK
13	100	34.1	807	1	RML_COTJA
14	100	34.1	849	1	SRK6_BRAOL
15	100	34.1	1080	1	NRK1_YEAST
16	100	34.1	1116	1	NRK1_YEAST
17	99	33.8	488	1	KI15_CAREL
18	98.5	33.6	974	1	CC15_YEAST
19	98	33.4	821	1	CTR1_ARATH
20	98	33.4	1097	1	KPC1_CANAL
21	98	33.4	1098	1	PGDR_MOUSE
22	97	33.1	1088	1	PGDS_RAT
23	97	33.1	1089	1	PGDS_HUMAN
24	97	33.1	1089	1	PGDS_MOUSE
25	96.5	32.9	490	1	SPS1_YEAST
26	96.5	32.9	821	1	SPK1_YEAST
27	96	32.8	1338	1	VGRI_YEAST
28	95.5	32.6	1307	1	PHY1_CERPU
29	95	32.4	443	1	ST24_HUMAN
30	95	32.4	506	1	MRK2_YEAST
31	95	32.4	801	1	FCR3_MOUSE
32	95	32.4	806	1	CEK2_CHICK
33	95	32.4	806	1	FCR3_HUMAN

34	95	32.4	812	1	FGRI_XENLA	P22182 xenopus lae
35	95	32.4	819	1	FGRI_CHICK	P21804 gallus gall
36	95	32.4	822	1	FGRI_HUMAN	P13662 mus sapien
37	95	32.4	822	1	FGRI_MOUSE	P16092 mus musculu
38	95	32.4	822	1	FGRI_RAT	004589 rattus norv
39	95	32.4	1087	1	PGDS_XENLA	P26619 xenopus lae
40	95	32.4	1106	1	PGDR_HUMAN	P09619 homo sapien
41	94	32.1	393	1	M3K7_DROME	P83104 drosophila
42	94	32.1	1333	1	PGDR_MOUSE	P35969 mus musculu
43	94	32.1	1336	1	VGRI_RAT	P53767 rattus norv
44	93	31.7	402	1	KROS_AVTISU	P00529 avian sarco
45	93	31.7	426	1	ST25_HUMAN	000506 homo sapien

## ALIGNMENTS

RESULT 1	M3K9_HUMAN	STANDARD:	PRT:	394 AA.
ID	M3K9_HUMAN			
AC	P80192:			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Mitogen-activated protein kinase kinase 9 (EC 2.7.1.-) (Mixed			
DE	lineage kinase 1) (Fragment).			
GN	MAP3K9 OR MKK1 OR PRKE1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE:Colon epithelium;			
RX	MEDLINE=9338756; PubMed=8477742;			
RA	Dorow D.S., Devereux L., Dietzsch E., de Kretser T.,			
RT	"Identification of a new family of human epithelial protein kinases			
RT	containing two leucine/isoleucine-zipper domains."			
RL	Eur. J. Biochem. 213:701-710(1993).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF			
CC	-1- COLONIC, BREAST AND OESOPHAGEAL ORIGIN.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	MAP KINASE KINASE SUBFAMILY.			
CC	PIR: S32467; S32467.			
DR	PIR: J00229; J00229.			
DR	HSSP: P12931; 1FMK.			
DR	Genev: HGNC:6861; MAP3K9.			
DR	MIM: 600136;			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	InterPro: IPR001245; Tyr_pkinase.			
DR	Pfam: PF00009; pkinase; 1.			
DR	Prodom: PD000001; Euk_pkinase; 1.			
DR	SMART: SM00219; TyrKc; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
KW	Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;			
KW	ATP-binding.			
FT	NON_TER	1		
FT	DOMAIN	3	271	PROTEIN KINASE.
FT	NE_BIND	9	17	ATP (BY SIMILARITY).
FT	ACT_SITE	127	127	ATP (BY SIMILARITY).
FT	DOMAIN	289	310	BY SIMILARITY.
FT	DOMAIN	324	345	LEUCINE-ZIPPER 1 (BY SIMILARITY).
FT	DOMAIN	354	368	LEUCINE-ZIPPER 2 (BY SIMILARITY).
FT	DOMAIN	368		ARG/LYS-RICH (BASIS).
SQ	SEQUENCE	394 AA:	44975 MW;	DBA0B/D3104/F88 CRC64;
Query Match	81.6%;	Score 239;	DB 1;	Length 394;
Best Local Similarity	77.8%;	Pred. No. 3.5e-22;		
Matches	42;	Conservative	7;	Mismatches 5; Indels 0; Gaps 0;

```

OY 1 HRDIFAGNILLLEKIEHDDICNKTITDFGLAREHMTTKMSAGTYAWMAPE 54
DB 125 HRDLKSSNILLLOKVENGDLSNKLITTFDGLAREHMTTKMSAGTYAWMAPE 178

RESULT 2
M3KA_HUMAN
ID M3KA_HUMAN STANDARD: PRT; 954 AA.
AC 002779; 012761; 014871;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
GN MAPK10 OR MKK2 OR MSK.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96128179; PubMed=8536694;
RA Dvorow D.S., Deyereux L., Tu G.F., Price G., Nicholl J.K.,
RA Sutherland G.R., Simpson R.J.;
RT "complete nucleotide sequence, expression, and chromosomal
RT localisation of human mixed-lineage kinase 2."
RL Eur. J. Biochem. 234:492-500(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95249256; PubMed=7731697;
RA Koth M., Hirai M., Sugimura T., Terada M.;
RT "cloning and characterization of MSK, a novel (putative)
RT serine/threonine kinase with SH3 domain."
RL Oncogene 10:1447-1451(1995).
RN [3]
RP SEQUENCE OF 244-480 FROM N.A.
RC TISSUE=Colon epithelium;
RX MEDLINE=93238756; PubMed=8477742;
RA Dvorow D.S., Deyereux L., Dietzsch E., de Kretser T.;
RT "identification of a new family of human epithelial protein kinases
RT containing two leucine/isoleucine-zipper domains."
RL Eur. J. Biochem. 213:701-710(1993).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
CC
CC EMBL; X90846; CAA62351.1; -
CC EMBL; Z48615; CAA88531.1; -
CC PIR; S32468; S32468.
CC HSSP; P13362; 1FGK.
CC Genew; HGNC:6849; MAP3K10.
CC MIM; 600137; -
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR004040; STY_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF000018; SH3_1.
CC Pfam; PF00069; Pkinase_1.
CC PRINTS; PR00452; SH3DOMAIN.
CC PRINTS; PR00109; TYRKINASE.

DR Prodom: PD000001; Euk_Pkinase; 1.
DR Prodom: PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50002; SH3; 1.
DR Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KM ATP-binding; SH3 domain.
FT DOMAIN 2 5 POLY-GLU.
FT DOMAIN 16 81 SH3.
FT DOMAIN 98 360 PROTEIN KINASE.
FT NP_BIND 104 112 ATP (BY SIMILARITY).
FT BINDING 125 125 ATP (BY SIMILARITY).
FT ACT_SITE 222 222 BY SIMILARITY.
FT DOMAIN 384 405 LEUCINE-ZIPPER 1 (BY SIMILARITY).
FT DOMAIN 419 440 LEUCINE-ZIPPER 2 (BY SIMILARITY).
FT DOMAIN 449 463 ARG/LYS-RICH (BASIC).
FT DOMAIN 462 464 SRL -> AV (IN REF. 2).
FT CONFLICT 465 480 LKREGSHSLPSGF -> AQAGRRPHPALWL (IN
FT REF. 3).
FT CONFLICT 471 471 G -> S (IN REF. 2).
FT CONFLICT 807 807 G -> R (IN REF. 2).
FT CONFLICT 818 818 V -> A (IN REF. 2).
SQ SEQUENCE 954 AA; 103623 MW; 538P4AA559B0A CRC64;

Query Match 73.7%; Score 216; DB 1; Length 954;
Beat Local Similarity 72.2%; Pred. No. 6.2e-19;
Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 HRDIFAGNILLLEKIEHDDICNKTITDFGLAREHMTTKMSAGTYAWMAPE 54
DB 220 HRDLKSSNILLLOKVENGDLSNKLITTFDGLAREHMTTKMSAGTYAWMAPE 273

RESULT 3
M3KC_HUMAN
ID M3KC_HUMAN STANDARD: PRT; 859 AA.
AC 012852;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)
DE (leucine-zipper protein kinase) (ZPK).
GN MAP3K12 OR ZPK.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Teraiocarcinoma;
RX MEDLINE=94311945; PubMed=8037767;
RA Reddy U.R., Pleasure D.;
RT "Cloning of a novel putative protein kinase having a leucine zipper
RT domain from human brain."
RL Blochem. Biophys. Res. Commun. 202:613-620(1994).
CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.
CC Phosphorylates beta-casein, histone 1 and myelin basic protein in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in brain and kidney.
CC -1- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
CC under basal conditions and dephosphorylated when membrane-
CC associated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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 CC -----  
 DR EMBL: U07358; AAA67343.1; -  
 DR HSSP: P12931; 1PMK.  
 DR Genew: HGNC:6851; MAP3K12.  
 DR MIM: 600447; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Magnesium; Membrane.  
 FT DOMAIN 125 366 PROTEIN\_KINASE.  
 FT NP\_BIND 131 139 APP (BY SIMILARITY).  
 FT BINDING 152 152 ATP (BY SIMILARITY).  
 FT ACT\_SITE 236 236 BY SIMILARITY.  
 FT DOMAIN 665 668 POLY-PRO.  
 FT DOMAIN 720 725 POLY-GLU.  
 SO SEQUENCE 859 AA; 93188 MW; 0E5209792C5C6F05 CRC64;  
 Query Match 42.5%; Score 124.5; DB 1; Length 859;  
 Best Local Similarity 50.9%; Pred. No. 1.1e-07;  
 Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;  
 Oy 1 HROIKAGNILLLEKIEHDDCNKTKITDGLAREW-HRTTKMSTAGTYAMAP 54  
 Db 234 HRDLKSPNML-----ITYDDV-----VKISDGTGSKELSDKSTKSPAGTYAMAP 280  
 RESULT 4  
 MKC\_MOUSE STANDARD; PRT; 888 AA.  
 AC 060700; P70286;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)  
 DE (leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing  
 DE kinase) (DLK).  
 GN MAP3K12 OR ZPK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Brain;  
 RA MEDLINE=95074107; PubMed=983011;  
 RA Holzman L.B., Merritt S.E., Fan G.;  
 RT "Identification, molecular cloning, and characterization of dual  
 RT leucine zipper bearing kinase. A novel serine/threonine protein kinase  
 RT that defines a second subfamily of mixed lineage kinases.";  
 RL J. Biol. Chem. 269:30808-30817(1994).  
 RU [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR X Swiss Webster; TISSUE=Brain;  
 RA MEDLINE=96365388; PubMed=8769565;  
 RA Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;  
 RT "Cell-specific expression of the zpk gene in adult mouse tissues.";  
 RL DNA Cell Biol. 15:631-642(1996).  
 RN [3]  
 RP PHOSPHORYLATION, AND MUTAGENESIS OF LYS-185 AND GLU-192.  
 RX MEDLINE=96279269; PubMed=8663324;

RA Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;  
 RT "Characterization of dual leucine zipper-bearing kinase, a mixed  
 RT lineage kinase present in synaptic terminals whose phosphorylation  
 RT state is regulated by membrane depolarization via calcineurin.";  
 RL J. Biol. Chem. 271:16888-16896(1996).  
 CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.  
 CC Phosphorylates beta-casein, histone 1 and myelin basic protein in  
 CC vitro.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -1- TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart,  
 CC testis, gastrointestinal tract, stomach, liver and pancreas.  
 CC Within the nervous system, predominantly expressed in neurons and  
 CC enriched in synaptic terminals.  
 CC -1- PMW: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol  
 CC under basal conditions and dephosphorylated when membrane-  
 CC associated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U14636; AAA57280.1; -  
 DR EMBL: U23789; AAB17123.1; -  
 DR HSSP: P12931; 1PMK.  
 DR MGD: MGI:1346881; Map3K12.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Magnesium; Membrane.  
 FT DOMAIN 158 399 PROTEIN\_KINASE.  
 FT NP\_BIND 164 172 APP (BY SIMILARITY).  
 FT BINDING 185 185 ATP.  
 FT ACT\_SITE 269 269 BY SIMILARITY.  
 FT DOMAIN 36 62 POLY-GLY.  
 FT DOMAIN 668 671 POLY-PRO.  
 FT DOMAIN 698 701 POLY-PRO.  
 FT DOMAIN 753 758 POLY-GLU.  
 FT MUTAGEN. 185 185 K->A: NO CATALYTIC ACTIVITY.  
 FT MUTAGEN. 192 192 E->A: NO CHANGE.  
 FT MUTAGEN. 192 192 V->A (IN REF. 2).  
 FT CONFLICT 16 18 KL->N (IN REF. 2).  
 FT CONFLICT 28 29 S->T (IN REF. 2).  
 FT CONFLICT 382 382 EQ->D (IN REF. 2).  
 FT CONFLICT 494 495 N->D (IN REF. 2).  
 FT CONFLICT 517 517 E->G (IN REF. 2).  
 FT CONFLICT 794 794 N->G (IN REF. 2).  
 SO SEQUENCE 888 AA; 96083 MW; CFECFD134F889AB CRC64;  
 Query Match 42.5%; Score 124.5; DB 1; Length 888;  
 Best Local Similarity 50.9%; Pred. No. 1.2e-07;  
 Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;  
 Oy 1 HROIKAGNILLLEKIEHDDCNKTKITDGLAREW-HRTTKMSTAGTYAMAP 54  
 Db 267 HRDLKSPNML-----ITYDDV-----VKISDGTGSKELSDKSTKSPAGTYAMAP 313  
 RESULT 5  
 MKC\_MOUSE STANDARD; PRT; 888 AA.  
 AC 060700; P70286;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)  
 DE (leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing  
 DE kinase) (DLK).  
 GN MAP3K12 OR ZPK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Brain;  
 RA MEDLINE=95074107; PubMed=983011;  
 RA Holzman L.B., Merritt S.E., Fan G.;  
 RT "Identification, molecular cloning, and characterization of dual  
 RT leucine zipper bearing kinase. A novel serine/threonine protein kinase  
 RT that defines a second subfamily of mixed lineage kinases.";  
 RL J. Biol. Chem. 269:30808-30817(1994).  
 RU [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR X Swiss Webster; TISSUE=Brain;  
 RA MEDLINE=96365388; PubMed=8769565;  
 RA Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;  
 RT "Cell-specific expression of the zpk gene in adult mouse tissues.";  
 RL DNA Cell Biol. 15:631-642(1996).  
 RN [3]  
 RP PHOSPHORYLATION, AND MUTAGENESIS OF LYS-185 AND GLU-192.  
 RX MEDLINE=96279269; PubMed=8663324;

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ID M3KC-RAT STANDARD: PRT: 888 AA.
AC 063796;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Mtopen-activated protein kinase kinase 12 (EC 2.7.1.37)
DE (MAPK-upstream kinase) (MUK).
GN MAP3K12 OR MUK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226099; PubMed=8637721;
RA Hirai S., Itawa M., Osada S., Spyrou G., Ohno S.;
RT "Activation of the JNK pathway by distantly related protein kinases,
RT MKK and MUK."
RL Oncogene 12:641-650(1996).
CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.
CC Phosphorylates beta-casein, histone H and myelin basic protein in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (by
CC similarity).
CC -1- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
CC under basal conditions and dephosphorylated when membrane-
CC associated (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: DA9785; BAA08621.1; -
DR HSSP: P12931; 1PMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Magnesium; Membrane.
FT DOMAIN 158 399 PROTEIN KINASE.
FT IN_BIND 164 172 ATP (BY SIMILARITY).
FT BINDING 185 185 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 BY SIMILARITY.
FT DOMAIN 56 62 POLY-GLY.
FT DOMAIN 668 671 POLY-PRO.
FT DOMAIN 698 701 POLY-PRO.
FT DOMAIN 753 758 POLY-GLU.
SQ SEQUENCE 888 AA; 96307 MW; 52AD964006BAE149 CRC64;

Query Match 42.5%; Score 124.5; DB 1; Length 888;
Best Local Similarity 50.9%; Pred. No. 1.2e-07;
Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;

```

```

OY 1 HRDIKAGNILLERIEHDICNKTITDGLAREW-HRTTKSTAGTAYAMAP 54
Db 267 HRDUKSPNML-----ITYDDV-----VKISDRGTSKELSDKSTKNSFGYVAMAP 313
RESULT 6

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ID BCK1_YEAST STANDARD: PRT: 1478 AA.
AC 001389; P32894;
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein kinase BCK1/SKL1/SSP31 (EC 2.7.1.37).
GN BCK1 OR SKL1 OR SSP31 OR IAS3 OR YJ1095W OR J0906.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92186847; PubMed=1545797;
RA Costigan C., Gehring S., Snyder M.;
RT "A synthetic lethal screen identifies SKL1, a novel protein kinase
RT homolog implicated in yeast cell morphogenesis and cell growth."
RL Mol. Cell. Biol. 12:1162-1178(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92104496; PubMed=1840547;
RA Irie K., Araki H., Oshima Y.;
RT "A new protein kinase, SSP31, modulating the SWP3 gene-product
RT involved in plasmid maintenance in Saccharomyces cerevisiae."
RL Gene 108:139-144(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=EG123;
RX MEDLINE=92107166; PubMed=1729597;
RA Lee K.S., Levin D.E.;
RT "Dominant mutations in a gene encoding a putative protein kinase
RT (BCK1) bypass the requirement for a Saccharomyces cerevisiae protein
RT kinase C homolog."
RL Mol. Cell. Biol. 12:1172-1182(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95176706; PubMed=7871887;
RA Miesha T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S.,
RA Zimmermann F.K.;
RT "Sequence and function analysis of a 9.74 kb fragment of
RT Saccharomyces cerevisiae chromosome X including the BCK1 gene."
RL Yeast 10:1481-1488(1994).
RN [5]
RP SEQUENCE OF 602-1104 FROM N.A.
RA Cusick M.E.;
RT Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SWP3; THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT ON THIS KINASE. BCK1 PROBABLY
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MPK1 KINASE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: M84389; -; NOT_ANNOTATED_CDS.
DR EMBL: D10389; BAA01226.1; -
DR EMBL: X60227; CAA42788.1; -
DR EMBL: X77823; CAA54896.1; -
DR EMBL: Z49370; CAA89389.1; -
DR EMBL: Z49369; CAA89388.1; -
DR EMBL: M88604; AAA21179.1; -

```

[illegible]

Best Local Similarity 51.8%; Pred. No. 6e-05;  
Matches 29; Conservative 5; Mismatches 12; Indels 10; Gaps 4;

OY 1 HRIKAGNILLEKIEHDDICKTKITDFTGL-AREHRTTKMST-AGTYAMAPE 54  
DB 432 HRIKSDNVL-----DMSGN-IKITDFGCARLSNRKRYTWGTPYMAPE 479

## RESULT 8

KRAB\_MOUSE STANDARD; PRF: 328 AA.  
AC P28028;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE B-RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)  
GN BRAF OR B-RAF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91271351; PubMed=2052597;  
RA Miki T., Fleming T.P., Crescenzi M., Molloy C.J., Blam S.B.,  
RA Reynolds S.H., Aaronson S.A.;  
RT "Development of a highly efficient expression cDNA cloning system:  
RT Application to oncogene isolation."  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5167-5171(1991).  
CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
CC -1- FROM THE CELL MEMBRANE TO THE NUCLEUS  
CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF  
CC HIPPOCAMPAL NEURON.  
CC -1- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES  
CC A T(11;22)(p11;p23) ONCOGENE ORIGINALLY ISOLATED FROM A FETAL  
CC INDUCED HEPATOMA.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC ML/RAF SUBFAMILY.

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CC -----  
DR EMBL: M64429; AAA37320.1; ALT\_INIT.  
DR PIR: A40951; TVMSBF.  
DR HSSP: P08631; IAD5.  
DR MGD: MGI:88190; Braf.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR004040; STY\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00221; STYKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR KMWATP-binding; serine/threonine-protein kinase; Proto-oncogene;  
KW ATP-binding; Chromosomal translocation.

FT DOMAIN 1 279  
FT NP\_BIND 25 33 PROTEIN KINASE.  
FT BINDING 45 45 ATP (BY SIMILARITY).  
FT ACT\_SITE 138 138 BY SIMILARITY.  
SQ SEQUENCE 328 AA; 36986 MW; 67A2EBFB78A7BE3D CRC64;

Query Match 34.1%; Score 100; DB 1; Length 328;  
Best Local Similarity 43.3%; Pred. No. 4.3e-05;  
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

OY 1 HRIKAGNILLEKIEHDDICKTKITDFTGL-AREHRTTKMST-AGTYAMAPE 54  
DB 136 HRIKSDNVL-----HEDL---TKITDFGCARLSNRKRYTWGTPYMAPE 185

## RESULT 9

RMIL\_AVII1 STANDARD; PRF: 367 AA.  
AC P10533; 085612; 085613; 085614;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine/threonine-protein kinase transforming protein Rml1  
DE (EC 2.7.1.37).  
GN V-RML1.  
OS Avian retrovirus IC10.  
OC Viruses; Retrovirus; Retroviridae; Avian type C retroviruses.  
OX NCBI\_Taxid=11874;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89160254; PubMed=2537952;  
RA Eychene A., Marx M., Dezeloe P., Calothy G.;  
RT "Complete nucleotide sequence of IC10, a retrovirus containing the  
RT Rml1 oncogene transduced in chicken neuroretina cells infected with  
RT avian retrovirus RAV-1."  
RL Nucleic Acids Res. 17:1250-1250(1989).

RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89091077; PubMed=2850163;  
RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,  
RA Dezeloe P., Pessac B., Calothy G.;  
RT "A novel oncogene related to c-mil is transduced in chicken  
RT neuroretina cells induced to proliferate by infection with an avian  
RT lymphomatous virus."  
RL EMO J. 7:3369-3373(1988).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL  
CC POLYPEPTIDE.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC ML/RAF SUBFAMILY.

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CC -----

DR EMBL: X13744; CAA32008.1; ALT\_SEQ.  
DR EMBL: X13438; CAA31790.1; ALT\_SEQ.  
DR PIR: S01645; TVEVM1.  
DR HSSP: P08631; IAD5.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR004040; STY\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00221; STYKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR KMWATP-binding; serine/threonine-protein kinase; Transferrase; Oncogene;  
KW ATP-binding.

FT DOMAIN 67 327  
FT NP\_BIND 73 81 PROTEIN KINASE.  
FT BINDING 93 93 ATP (BY SIMILARITY).  
FT ACT\_SITE 186 186 BY SIMILARITY.  
SQ SEQUENCE 367 AA; 41023 MW; 5137ARCDBC8398A CRC64;

Query Match 34.1%; Score 100; DB 1; Length 367;  
Best Local Similarity 43.3%; Pred. No. 4.8e-05;

Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;  
 1 HRDRAAGNILLLEKIEHDIKCNKTLKITDFGLA---RWM---HRTTKMSTAGTYAMMAPE 54  
 184 HRDLKSNINFL-----HEDL---TVKIDGFLATYKSRMSGSHQEQOLS--GSILWMAPE 233

## RESULT 10

RMLL\_AVEVR  
 ID RMLL\_AVEVR STANDARD: PRT: 450 AA.  
 AC P27966;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase transforming protein Rml1  
 DE (EC 2.7.1.37).  
 GN V-RML1.  
 OS Avian rous-associated virus type 1.  
 OC Viruses; Retrovirda; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11950;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91251215; PubMed=1645786;  
 RA Felder M.P., Eychene A., Barnier J.V., Calogeraki I., Calothy G.,  
 RT "Common mechanism of retrovirus activation and transduction of c-mil  
 RT and c-Rml1 in chicken neuroretina cells infected with Rous-associated  
 RT virus type 1."  
 RL J. Virol. 65:3633-3640(1991).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV  
 CC POLYPROTEIN. BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.

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 CC -----  
 DR EMBL: M62407; AAA42549.1; -  
 DR PIR: A40341; TVFVNR.  
 DR HSP: P08631; 14D5.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Polyprotein: Serine/threonine-protein kinase; Transferase; Oncogene;  
 KW ATP-binding.  
 KW DOMAIN 83 343 PROTEIN KINASE.  
 FT NP\_BIND 89 97 ATP (BY SIMILARITY).  
 FT BINDING 109 109 ATP (BY SIMILARITY).  
 FT ACT\_SITE 202 202 BY SIMILARITY.  
 SQ SEQUENCE 450 AA; 50313 MM; 6581AAAF2253CB622 CRC64;

Query Match 34.1%; Score 100; DB 1; Length 450;  
 Best Local Similarity 43.3%; Pred. No. 6e-05; Indels 16; Gaps 5;  
 Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

OY 1 HRDRAAGNILLLEKIEHDIKCNKTLKITDFGLA---RWM---HRTTKMSTAGTYAMMAPE 54  
 184 HRDLKSNINFL-----HEDL---TVKIDGFLATYKSRMSGSHQEQOLS--GSILWMAPE 249

RESULT 11

KRAB\_HUMAN  
 ID KRAB\_HUMAN STANDARD: PRT: 765 AA.

AC P15056;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE B-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)  
 DE (p94) (V-Raf murine sarcoma viral oncogene homolog B1).  
 GN BRAF OR BRAF1 OR KAPB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Testis;  
 RX MEDLINE=92375040; PubMed=1508179;  
 RA Stephens R.M., Sithanandam G., Copeland T.D., Kaplan D.R., Rapp U.R.,  
 RA Morrison D.K.;  
 RT "95-kilodalton B-Raf serine/threonine kinase: identification of the  
 RT protein and its major autophosphorylation site."  
 RT Mol. Cell. Biol. 12:3733-3742(1992).  
 RL [2]  
 RN  
 RP SEQUENCE OF 116-765 FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=91133728; PubMed=2284096;  
 RA Sithanandam G., Kolch W., Duh F.-M., Rapp U.R.;  
 RT "Complete coding sequence of a human B-Raf cDNA and detection of  
 RT B-Raf protein kinase with isozyme specific antibodies."  
 RT Oncogene 5:1775-1780(1990).  
 RL [3]  
 RN  
 RP SEQUENCE OF 438-765 FROM N.A.  
 RX MEDLINE=88302178; PubMed=3043188;  
 RA Ikawa S., Fukui M., Ueyama Y., Tamaki N., Yamamoto T., Toyoshima K.;  
 RT "B-Raf, a new member of the raf family, is activated by DNA  
 RT rearrangement."  
 RL Mol. Cell. Biol. 8:2651-2654(1988).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.  
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF  
 CC HIPPOCAMPAL NEURON.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: CEREBRUM AND TESTES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHOSPHO-ESTER AND DAG  
 CC BINDING DOMAIN.

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 CC -----  
 DR EMBL: M95712; AAA35609.1; -  
 DR EMBL: M21001; AAA96495.1; -  
 DR PIR: A31850; TVHUBF.  
 DR PIR: S13798; S13798.  
 DR HSP: P04049; 1FAR.  
 DR Genew: HGNC:1097; BRAF.  
 DR MIM: 164757; -  
 DR InterPro: IPR002219; DAG\_PE\_bind.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003116; RBD.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR Pfam: PF00130; DAG\_PE\_bind; 1.  
 DR Pfam: PF02196; RBD; 1.  
 DR PRINTS: PR00008; DAGPEDOMAIN.  
 DR ProDom: PD000001; Euk\_pkinase; 1.



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DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding; Phosphorylation.
FT DOMAIN 6 11 POLY-SER.
FT DOMAIN 121 128 POLY-SER.
FT DOMAIN 234 279 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 427 431 POLY-SER.
FT NP_BIND 456 476 PROTEIN KINASE.
FT BINDING 462 482 ATP (BY SIMILARITY).
FT ACT_SITE 575 575 ATP (BY SIMILARITY).
FT MOD_RES 372 372 BY SIMILARITY.
FT CONFLICT 765 765 H->D (IN REF. 3).
SO SEQUENCE 765 AA; 84490 MW; 93A9EEED6C1C68E CRC64;

Query Match 34.1%; Score 100; DB 1; Length 765;
Best Local Similarity 43.3%; Pred. No. 0.0001;
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDIKAGNILLLEKIEHDDICNKLTKITDGLA---REW---HRTTKMSTAGTYAMWAP 54
Db 573 HRDIKSNINFL-----HEDL---TVKIDFGLATVKSRSMSGSHOEPQLS--GSTIMWAP 622

RESULT 12
RMIL_CHICK STANDARD; PRT; 806 AA.
ID RMIL_CHICK
AC C04982;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).
GN C-RMIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes, and Fibroblast;
RX MEDLINE=93312327; PubMed=8323553;
RA Calogeraki I., Barnier J.V., Eychene A., Felder M.-P., Calothy G.,
RA Marx M.,
RT "Genomic organization and nucleotide sequence of the coding region of
RT the chicken c-RmIL(B-raf-1) proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC NEURAL CELLS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC ML/RAE SUPFAMILY.
CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -----
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CC -----
CC EMBL; X67052; CAA47436.1; -.
CC PIR; J0612; J0612.
CC HSSP; P04049; IPEAR.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR pfam; PF00069; pkinase; 1.
DR pfam; PF00130; DAG_PE-bind; 1.
DR pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW Proto-oncogene; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
KW Phorbol-ester binding; Phosphorylation.
FT DOMAIN 122 129 POLY-SER.
FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 248 260 CYS-RICH.
FT DOMAIN 497 757 PROTEIN KINASE.
FT NP_BIND 503 511 ATP (BY SIMILARITY).
FT BINDING 523 523 ATP (BY SIMILARITY).
FT ACT_SITE 616 616 BY SIMILARITY.
FT VARSPIC 393 432 MISSING (IN SHORT ISOFORM).
SO SEQUENCE 806 AA; 89365 MW; 8F3FAD5274FB75C CRC64;

Query Match 34.1%; Score 100; DB 1; Length 806;
Best Local Similarity 43.3%; Pred. No. 0.0001;
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDIKAGNILLLEKIEHDDICNKLTKITDGLA---REW---HRTTKMSTAGTYAMWAP 54
Db 614 HRDIKSNINFL-----HEDL---TVKIDFGLATVKSRSMSGSHOEPQLS--GSTIMWAP 663

RESULT 13
RMIL_COTUJA STANDARD; PRT; 807 AA.
ID RMIL_COTUJA
AC P34908;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).
GN C-RMIL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92319540; PubMed=1620546;
RX Eychene A., Barnier J.V., Dezelic P., Marx M., Laugier D.,
RA Calogeraki I., Calothy G.,
RT "Quali neurorretina c-RmIL(B-raf) proto-oncogene cDNAs encode two
RT proteins of 93.5 and 95 kDa resulting from alternative splicing.";
RL Oncogene 7:1315-1323(1992).
CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC NEURAL CELLS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

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